

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Gorski, David H.
Walsh, Kenneth
- (ii) TITLE OF INVENTION: Growth Arrest Homeobox Gene
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Calfee, Halter, and Griswold
(B) STREET: 800 Superior Avenue
(C) CITY: Cleveland
(D) STATE: Ohio
(E) COUNTRY: U.S.A.
(F) ZIP: 44114-2688
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Golrick, Mary E.
(B) REGISTRATION NUMBER: 34829
(C) REFERENCE/DOCKET NUMBER: 22311/00114
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (216) 622-8200
(B) TELEFAX: (216) 241-0816
(C) TELEX: 980499

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2244 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 197..1108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCAAGTGTGTT TATACGTGCA GGAGACTGGC CGCTCGGCTC AGGACTGGGA TTAGCGGGCT
60

22311/00114

34

CTGCTCAAAC CCGCGCGGCT TTTACATTAG GAGTGAGTGG GGGAGAGTCC TAGGATTTCT
120

AGTGAAAAGT GACAGCGCTT GGTGGACTTT GGGACCTTCG TGAAGTCTTC TGCTTGAAG
180

CTGAGACTTG CATGCC ATG GAA CAC CCC CTC TTT GGC TGC CTG CGC AGC
229

Met Glu His Pro Leu Phe Gly Cys Leu Arg Ser
1 5 10

CCC CAC GCC ACA GCG CAA GGC TTG CAC CCC TTC TCG CAG TCT TCT CTG
277

Pro His Ala Thr Ala Gln Gly Leu His Pro Phe Ser Gln Ser Ser Leu
15 20 25

GCC CTC CAT GGA AGA TCT GAC CAC ATG TCC TAC CCC GAA CTC TCC ACA
325

Ala Leu His Gly Arg Ser Asp His Met Ser Tyr Pro Glu Leu Ser Thr
30 35 40

TCT TCC TCG TCT TGC ATA ATC GCG GGA TAC CCC AAT GAG GAG GGC ATG
373

Ser Ser Ser Ser Cys Ile Ile Ala Gly Tyr Pro Asn Glu Glu Gly Met
45 50 55

TTT GCC AGC CAG CAT CAC AGG GGG CAC CAC CAC CAC CAC CAC CAC CAC
421

Phe Ala Ser Gln His His Arg Gly His His His His His His His His
60 65 70 75

CAT CAC CAC CAC CAG CAG CAG CAG CAC CAG GCT CTG CAA AGC AAC TGG
469

His His His His Gln Gln Gln Gln His Gln Ala Leu Gln Ser Asn Trp
80 85 90

CAC CTC CCG CAG ATG TCC TCC CCG CCA AGC GCG GCC CGG CAC AGC CTT
517

His Leu Pro Gln Met Ser Ser Pro Pro Ser Ala Ala Arg His Ser Leu
95 100 105

TGC CTG CAG CCT GAT TCC GGA GGG CCC CCG GAG CTG GGG AGC AGC CCT
565

Cys Leu Gln Pro Asp Ser Gly Gly Pro Pro Glu Leu Gly Ser Ser Pro
110 115 120

CCG GTC CTG TGC TCC AAC TCT TCT AGC CTG GGC TCC AGC ACC CCG ACC
613

Pro Val Leu Cys Ser Asn Ser Ser Ser Leu Gly Ser Ser Thr Pro Thr
125 130 135

GGA GCC GCG TGC GCA CCA AGG GAT TAT GGC CGT CAA GCG CTG TCA CCC
661

Gly Ala Ala Cys Ala Pro Arg Asp Tyr Gly Arg Gln Ala Leu Ser Pro
140 145 150 155

GCA GAA GTG GAG AAG AGA AGT GGC AGC AAA AGA AAA AGC GAC AGT TCA
709

Ala Glu Val Glu Lys Arg Ser Gly Ser Lys Arg Lys Ser Asp Ser Ser
160 165 170

GAT TCC CAG GAA GGA AAT TAC AAG TCA GAA GTG AAC AGC AAA CCT AGG
757

Asp Ser Gln Glu Gly Asn Tyr Lys Ser Glu Val Asn Ser Lys Pro Arg
175 180 185

AGG GAA AGA ACA GCT TTC ACC AAA GAG CAA ATC AGA GAA CTT GAG GCA

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Gorski, David H.
Walsh, Kenneth
- (ii) TITLE OF INVENTION: Growth Arrest Homeobox Gene
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Calfee, Halter, and Griswold
(B) STREET: 800 Superior Avenue
(C) CITY: Cleveland
(D) STATE: Ohio
(E) COUNTRY: U.S.A.
(F) ZIP: 44114-2688
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Golrick, Mary E.
(B) REGISTRATION NUMBER: 34829
(C) REFERENCE/DOCKET NUMBER: 22311/00114
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (216) 622-8200
(B) TELEFAX: (216) 241-0816
(C) TELEX: 980499

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2244 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 197..1108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCAAGTGTT TATACGTGCA GGAGACTGGC CGCTCGGCTC AGGACTGGGA TTAGCGGGCT
60

22311/00114

34

CTGCTCAAAC CCGCGCGGCT TTTACATTAG GAGTGAGTGG GGGAGAGTCC TAGGATTTCT
120

AGTGAAAAGT GACAGCGCTT GGTGGACTTT GGGACCTTCG TGAAGTCTTC TGCTTGGAAG
180

CTGAGACTTG CATGCC ATG GAA CAC CCC CTC TTT GGC TGC CTG CGC AGC
229

Met Glu His Pro Leu Phe Gly Cys Leu Arg Ser
1 5 10

CCC CAC GCC ACA GCG CAA GGC TTG CAC CCC TTC TCG CAG TCT TCT CTG
277

Pro His Ala Thr Ala Gln Gly Leu His Pro Phe Ser Gln Ser Ser Leu
15 20 25

GCC CTC CAT GGA AGA TCT GAC CAC ATG TCC TAC CCC GAA CTC TCC ACA
325

Ala Leu His Gly Arg Ser Asp His Met Ser Tyr Pro Glu Leu Ser Thr
30 35 40

TCT TCC TCG TCT TGC ATA ATC GCG GGA TAC CCC AAT GAG GAG GGC ATG
373

Ser Ser Ser Ser Cys Ile Ile Ala Gly Tyr Pro Asn Glu Glu Gly Met
45 50 55

TTT GCC AGC CAG CAT CAC AGG GGG CAC CAC CAC CAC CAC CAC CAC
421

Phe Ala Ser Gln His His Arg Gly His His His His His His His
60 65 70 75

CAT CAC CAC CAC CAG CAG CAG CAG CAC CAG GCT CTG CAA AGC AAC TGG
469

His His His His Gln Gln Gln Gln His Gln Ala Leu Gln Ser Asn Trp
80 85 90

CAC CTC CCG CAG ATG TCC TCC CCG CCA AGC GCG GCC CGG CAC AGC CTT
517

His Leu Pro Gln Met Ser Ser Pro Pro Ser Ala Ala Arg His Ser Leu
95 100 105

TGC CTG CAG CCT GAT TCC GGA GGG CCC CCG GAG CTG GGG AGC AGC CCT
565

Cys Leu Gln Pro Asp Ser Gly Gly Pro Pro Glu Leu Gly Ser Ser Pro
110 115 120

CCG GTC CTG TGC TCC AAC TCT TCT AGC CTG GGC TCC AGC ACC CCG ACC
613

Pro Val Leu Cys Ser Asn Ser Ser Ser Leu Gly Ser Ser Thr Pro Thr
125 130 135

GGA GCC GCG TGC GCA CCA AGG GAT TAT GGC CGT CAA GCG CTG TCA CCC
661

Gly Ala Ala Cys Ala Pro Arg Asp Tyr Gly Arg Gln Ala Leu Ser Pro
140 145 150 155

GCA GAA GTG GAG AAG AGA AGT GGC AGC AAA AGA AAA AGC GAC AGT TCA
709

Ala Glu Val Glu Lys Arg Ser Gly Ser Lys Arg Lys Ser Asp Ser Ser
160 165 170

GAT TCC CAG GAA GGA AAT TAC AAG TCA GAA GTG AAC AGC AAA CCT AGG
757

Asp Ser Gln Glu Gly Asn Tyr Lys Ser Glu Val Asn Ser Lys Pro Arg
175 180 185

AGG GAA AGA ACA GCT TTC ACC AAA GAG CAA ATC AGA GAA CTT GAG GCA

805

Arg Glu Arg Thr Ala Phe Thr Lys Glu Gln Ile Arg Glu Leu Glu Ala
 190 195 200

5

GAG TTC GCC CAT CAT AAC TAT CTG ACC AGA CTG AGA AGA TAT GAG ATA
 853
 Glu Phe Ala His His Asn Tyr Leu Thr Arg Leu Arg Arg Tyr Glu Ile
 205 210 215

10

GCG GTG AAC CTA GAC CTC ACT GAA AGA CAG GTG AAA GTG TGG TTC CAG
 901
 Ala Val Asn Leu Asp Leu Thr Glu Arg Gln Val Lys Val Trp Phe Gln
 220 225 230 235

15

AAC AGG AGA ATG AAG TGG AAG CGG GTC AAG GGG GGA CAA CAA GGA GCT
 949
 Asn Arg Arg Met Lys Trp Lys Arg Val Lys Gly Gly Gln Gln Gly Ala
 240 245 250

20

GCA GCC CGA GAA AAG GAA CTG GTG AAT GTG AAA AAG GGA ACA CTT CTT
 997
 Ala Ala Arg Glu Lys Glu Leu Val Asn Val Lys Lys Gly Thr Leu Leu
 255 260 265

25

CCA TCA GAG CTG TCA GGA ATT GGT GCA GCC ACC CTC CAG CAG ACA GGG
 1045
 Pro Ser Glu Leu Ser Gly Ile Gly Ala Ala Thr Leu Gln Gln Thr Gly
 270 275 280

30

GAC TCA CTA GCA AAT GAC GAC AGT CGC GAT AGT GAC CAC AGC TCT GAG
 1093
 Asp Ser Leu Ala Asn Asp Asp Ser Arg Asp Ser Asp His Ser Ser Glu
 285 290 295

35

CAC GCA CAC TTA TGATACATAC AGAGACCAGC TCCGTTCTCA GGAAAGCACC
 1145
 His Ala His Leu
 300

40

ATTGTGATGG CAAATCTCAC CCAAACATCG TTTACATGGC AGATGACTGT GGCAGTGTG
 1205

CTTAATATAA TTAAACGCAG GCATCTCAAG TCTGTTTCTC ATGATTGATA GAAGGTTTAC
 1265

45

ACTAAGTGCC TCTTATTGAA GATGCTTCCA CAGTGAAATT GGAGAAAGTG AACATATCTA
 1325

50

AATATACTTG TTCCTTATAT GACAGAGAGG GAGATGAATG TTTGCTTTGG CTTGCACTGA
 1385

AAATTAAATT GCTACCAAGA GCAAACCTCG TAAGACATTT TGAATCAAGT TGTCTCCAGA
 1445

55

GTGAAGATGT TATAGAAATG CTTTGAACAT TCCAGTTGTA CCAGGTCATG TGTGTGACAC
 1505

TGGGCAGGTA TTTGCTTTTG CTTGCACTGA AACTTAAACT GCTATCAAGT TAACCCATGA
 1565

60

AATAGTTTAT CTTGAACAGC CACAGTGCCT GAAATCACCA AGTGGATATA AAATGAACTG
 1625

65

AAATTCTGTA TATATTACTC CTAAGTCATT TTCCTGTCTT CACTAATTTT AGCAAATGCA
 1685

TTCATATTAG CTGATGAAAA TAGGCTTTCC CGTGGACAAA TGCAGCCAGC TTCTTGATT

1745

TTTATACATT TTTTGTGTCAG TCAGAGACAT CAGTATGTGC TTACTTGTGT TCAAGTAGAG
1805

GAAATGCAGT AGAGTCTGAT AGGACATATT CTTGGTACCA CAGACAAAAC AAATCTTCTG
1865

TTGCATTGAC TATCAACTGC TGCAGATACA TTAGAGAACA CACCTAGCCC CCCTCCAGCC
1925

TCCCTCTGTT ATCGCTCGAA GACATTAGCG TCATAGGCAA GTAGTTACCT TGCCAAATGA
1985

GTCTTGTGTG GCAGATGTCT GATTTTGTAT CTTTAACTG TTAATGGTAT GTGTCTGCTT
2045

CAGTTAACAG GGAAAAAGAT TTCTTCCTCA TTGTTTATGA TACAAAACCC AAGTGCCAAA
2105

CAAAGCTAGT TCTTCAAGGG ATAGATGAGA AACTGAATGT CTGACAAGTA GACTCAGCGA
2165

AAATACATTA TTTTTCAGAG GCTGTGTATT CATGCAGTAC AAGTCCTTGT ATTTTGTAAA
2225

AAAAAAAAGTT AAATAAATG
2244

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Glu	His	Pro	Leu	Phe	Gly	Cys	Leu	Arg	Ser	Pro	His	Ala	Thr	Ala	1	5	10	15
Gln	Gly	Leu	His	Pro	Phe	Ser	Gln	Ser	Ser	Leu	Ala	Leu	His	Gly	Arg	20	25	30	
Ser	Asp	His	Met	Ser	Tyr	Pro	Glu	Leu	Ser	Thr	Ser	Ser	Ser	Ser	Cys	35	40	45	
Ile	Ile	Ala	Gly	Tyr	Pro	Asn	Glu	Glu	Gly	Met	Phe	Ala	Ser	Gln	His	50	55	60	
His	Arg	Gly	His	His	His	His	His	His	His	His	His	His	His	His	Gln	65	70	75	80
Gln	Gln	Gln	His	Gln	Ala	Leu	Gln	Ser	Asn	Trp	His	Leu	Pro	Gln	Met	85	90	95	
Ser	Ser	Pro	Pro	Ser	Ala	Ala	Arg	His	Ser	Leu	Cys	Leu	Gln	Pro	Asp	100	105	110	
Ser	Gly	Gly	Pro	Pro	Glu	Leu	Gly	Ser	Ser	Pro	Pro	Val	Leu	Cys	Ser	115	120	125	
Asn	Ser	Ser	Ser	Leu	Gly	Ser	Ser	Thr	Pro	Thr	Gly	Ala	Ala	Cys	Ala	130	135	140	

22311/00114

37

Pro Arg Asp Tyr Gly Arg Gln Ala Leu Ser Pro Ala Glu Val Glu Lys
145 150 155 160

Arg Ser Gly Ser Lys Arg Lys Ser Asp Ser Ser Asp Ser Gln Glu Gly
165 170 175

Asn Tyr Lys Ser Glu Val Asn Ser Lys Pro Arg Arg Glu Arg Thr Ala
180 185 190

Phe Thr Lys Glu Gln Ile Arg Glu Leu Glu Ala Glu Phe Ala His His
195 200 205

Asn Tyr Leu Thr Arg Leu Arg Arg Tyr Glu Ile Ala Val Asn Leu Asp
210 215 220

Leu Thr Glu Arg Gln Val Lys Val Trp Phe Gln Asn Arg Arg Met Lys
225 230 235 240

Trp Lys Arg Val Lys Gly Gly Gln Gln Gly Ala Ala Ala Arg Glu Lys
245 250 255

Glu Leu Val Asn Val Lys Lys Gly Thr Leu Leu Pro Ser Glu Leu Ser
260 265 270

Gly Ile Gly Ala Ala Thr Leu Gln Gln Thr Gly Asp Ser Leu Ala Asn
275 280 285

Asp Asp Ser Arg Asp Ser Asp His Ser Ser Glu His Ala His Leu
290 295 300

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 941 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 33..941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTCTTCTACC TGGAACCCGA AACTTGCATG CT ATG GAA CAC CCG CTC TTT GGC
53

Met Glu His Pro Leu Phe Gly
1 5

TGC CTG CGC AGC CCT CAC GCC ACG GCG CAA GGC TTG CAC CCG TTC TCC
101

Cys Leu Arg Ser Pro His Ala Thr Ala Gln Gly Leu His Pro Phe Ser
10 15 20

CAA TCC TCT CTC GCC CTC CAT GGA AGA TCT GAC CAT ATG TCT TAC CCC
149

Gln Ser Ser Leu Ala Leu His Gly Arg Ser Asp His Met Ser Tyr Pro
25 30 35

GAG CTC TCT ACT TCT TCC TCA TCT TGC ATA ATC GCG GGA TAC CCC AAC
 197
 Glu Leu Ser Thr Ser Ser Ser Ser Cys Ile Ile Ala Gly Tyr Pro Asn
 40 45 50 55
 GAA GAG GAC ATG TTT GCC AGC CAG CAT CAC AGG GGG CAC CAC CAC CAC
 245
 Glu Glu Asp Met Phe Ala Ser Gln His His Arg Gly His His His His
 60 65 70
 CAC CAC CAC CAT CAC CAC CAT CAG CAG CAG CAG CAC CAG GCT CTG CAA
 293
 His His His His His His His Gln Gln Gln Gln His Gln Ala Leu Gln
 75 80 85
 ACC AAC TGG CAC CTC CCG CAG ATG TCT TCC CCA CCG AGT GCG GCT CGG
 341
 Thr Asn Trp His Leu Pro Gln Met Ser Ser Pro Pro Ser Ala Ala Arg
 90 95 100
 CAT AGC CTC TGC CTC CAG CCC GAC TCT GGA GGG CCC CCA GAG TTG GGG
 389
 His Ser Leu Cys Leu Gln Pro Asp Ser Gly Gly Pro Pro Glu Leu Gly
 105 110 115
 AGC AGC CCG CCC GTC CTG TGC TCC AAC TCT TCC AGC TTG GGC TCC AGC
 437
 Ser Ser Pro Pro Val Leu Cys Ser Asn Ser Ser Ser Leu Gly Ser Ser
 120 125 130 135
 ACC CCG ACT GGG GCC GCG TGC GCG CCG GGG GAC TAC GGC CGC CAG GCA
 485
 Thr Pro Thr Gly Ala Ala Cys Ala Pro Gly Asp Tyr Gly Arg Gln Ala
 140 145 150
 CTG TCA CCT GCG GAG GCG GAG AAG CGA AGC GGC GGC AAG AGG AAA AGC
 533
 Leu Ser Pro Ala Glu Ala Glu Lys Arg Ser Gly Gly Lys Arg Lys Ser
 155 160 165
 GAC AGC TCA GAC TCC CAG GAA GGA AAT TAC AAG TCA GAA GTC AAC AGC
 581
 Asp Ser Ser Asp Ser Gln Glu Gly Asn Tyr Lys Ser Glu Val Asn Ser
 170 175 180
 AAA CCC AGG AAA GAA AGG ACA GCA TTT ACC AAA GAG CAA ATC AGA GAA
 629
 Lys Pro Arg Lys Glu Arg Thr Ala Phe Thr Lys Glu Gln Ile Arg Glu
 185 190 195
 CTT GAA GCA GAA TTT GCC CAT CAT AAT TAT CTC ACC AGA CTG AGG CGA
 677
 Leu Glu Ala Glu Phe Ala His His Asn Tyr Leu Thr Arg Leu Arg Arg
 200 205 210 215
 TAC GAG ATA GCA GTG AAT CTG GAT CTC ACT GAA AGA CAG GTA AAA GTC
 725
 Tyr Glu Ile Ala Val Asn Leu Asp Leu Thr Glu Arg Gln Val Lys Val
 220 225 230
 TGG TTC CAA AAC AGG CGG ATG AAG TGG AAG AGG GTA AAG GGT GGA CAG
 773
 Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Arg Val Lys Gly Gly Gln
 235 240 245
 CAA GGA GCT GCG GCT CGG GAA AAG GAA CTG GTG AAT GTG AAA AAG GGA
 821

Gln Gly Ala Ala Ala Arg Glu Lys Glu Leu Val Asn Val Lys Lys Gly
250 255 260

ACA CTT CTC CCA TCA GAG CTG TCG GGA ATT GGT GCA GCC ACC CTC CAG
869

Thr Leu Leu Pro Ser Glu Leu Ser Gly Ile Gly Ala Ala Thr Leu Gln
265 270 275

CAA ACA GGG GAC TCT ATA GCA AAT GAA GAC AGT CAC GAC AGT GAC CAC
917

Gln Thr Gly Asp Ser Ile Ala Asn Glu Asp Ser His Asp Ser Asp His
280 285 290 295

AGC TCA GAG CAC GCC CAC CTC TGA
941

Ser Ser Glu His Ala His Leu
300

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 302 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Glu His Pro Leu Phe Gly Cys Leu Arg Ser Pro His Ala Thr Ala
1 5 10 15

Gln Gly Leu His Pro Phe Ser Gln Ser Ser Leu Ala Leu His Gly Arg
20 25 30

Ser Asp His Met Ser Tyr Pro Glu Leu Ser Thr Ser Ser Ser Cys
35 40 45

Ile Ile Ala Gly Tyr Pro Asn Glu Glu Asp Met Phe Ala Ser Gln His
50 55 60

His Arg Gly His His His His His His His His His His His Gln Gln
65 70 75 80

Gln Gln His Gln Ala Leu Gln Thr Asn Trp His Leu Pro Gln Met Ser
85 90 95

Ser Pro Pro Ser Ala Ala Arg His Ser Leu Cys Leu Gln Pro Asp Ser
100 105 110

Gly Gly Pro Pro Glu Leu Gly Ser Ser Pro Pro Val Leu Cys Ser Asn
115 120 125

Ser Ser Ser Leu Gly Ser Ser Thr Pro Thr Gly Ala Ala Cys Ala Pro
130 135 140

Gly Asp Tyr Gly Arg Gln Ala Leu Ser Pro Ala Glu Ala Glu Lys Arg
145 150 155 160

Ser Gly Gly Lys Arg Lys Ser Asp Ser Ser Asp Ser Gln Glu Gly Asn
165 170 175

Tyr Lys Ser Glu Val Asn Ser Lys Pro Arg Lys Glu Arg Thr Ala Phe
180 185 190

Thr Lys Glu Gln Ile Arg Glu Leu Glu Ala Glu Phe Ala His His Asn

22311/00114

40

195

200

205

Tyr Leu Thr Arg Leu Arg Arg Tyr Glu Ile Ala Val Asn Leu Asp Leu
210 215 220

Thr-Glu Arg Gln Val Lys Val Trp Phe Gln Asn Arg Arg Met Lys Trp
225 230 235 240

Lys Arg Val Lys Gly Gly Gln Gln Gly Ala Ala Ala Arg Glu Lys Glu
245 250 255

Leu Val Asn Val Lys Lys Gly Thr Leu Leu Pro Ser Glu Leu Ser Gly
260 265 270

y
Ile Gly Ala Ala Thr Leu Gln Gln Thr Gly Asp Ser Ile Ala Asn Glu
275 280 285

Asp Ser His Asp Ser Asp His Ser Ser Glu His Ala His Leu
290 295 300

FOIA b 7 - D